

[REDACTED]

## SUMMARIES

Result	No.	Score	Query Match	Length	DB ID	Description
c	1	925	100.0	925	14	Sequence 3, Appli
c	2	59.6	6.4	925	14	Sequence 3, Appli
c	3	45.8	5.0	10328	12	Sequence 1518, Ap
c	4	44	4.8	3673778	12	Sequence 2, Appli
c	5	43.6	4.7	9524	12	Sequence 812, App
c	6	42.6	4.6	18817	12	Sequence 48, Appli
c	7	42.2	4.6	10254	12	Sequence 1048, Ap
c	8	41.6	4.5	7676	12	Sequence 152, App
c	9	41.4	4.5	17594	12	Sequence 1399, Ap
c	10	41.2	4.5	6275	12	Sequence 524, App
c	11	41	4.4	5488	12	Sequence 1429, Ap
c	12	41	4.4	5930	12	Sequence 1368, Ap
c	13	40.8	4.4	88	12	Sequence 108, App
c	14	40.6	4.4	2000	10	Sequence 5309, Ap
c	15	40.6	4.4	9427	12	Sequence 1571, Ap
c	16	40.6	4.4	9927	12	Sequence 85, Appli

## ALIGNMENTS

## RESULT 7

US-10-039-836A-3

: Sequence 3, Application US/10039836A

; Publication No. US20030033632A1

; GENERAL INFORMATION:

APPLICANT: Crane, Virginia

**TITLE OF INVENTION:** Maize proteinase inhibitor-like

**TITLE OF INVENTION:** Polynuc

; FILE REFERENCE: 35718/239836

; CURRENT APPLICATION NUMBER: US/1

; CURRENT FILING DATE: 2001-10-23 167  
 ; PRIORITY APPLICATION NUMBER: 60/243 167

: PRIOR FILING DATE: 2000-10-25  
 : PRIOR APPLICATION NUMBER: 00/243,107

NUMBER OF SEO ID NOS: 4

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 3

;; LENGTH: 925  
TYPE: ONE

TYPE: DNA  
ORGANISM: 700 mays

ORGANISM: zed ways  
FEATURE:

```
;; NAME/KEY: misc_feature
```

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; LOCATION: (0)...(0)

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OTHER INFORMATION: Proteinase Inhibitor

US-10-039-836A-3

Query Match	100 %	Score 925
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Query match	100.0%;	Score 323
Best Local Similarity	100.08;	pred. No.

Matches 925; Conservative 0; Mismatch

1 ACTATAGGGCACGGCTGGTCGACGGCCCGG QY

[illegible]

DD I ACIAAGGGCAAGCGTGGTGGACGGCCCGG

61 TGTATGGGTACCCCCCTTATACGATTGCC



61 TGTGATGGGTCAGCCCCCTTATACGATTGCC

E  
 E  
 C  
 E  
 C  
 E  
 C  
 E  
 C  
 A  
 C  
 E  
 A  
 C  
 E  
 C  
 A  
 C  
 C  
 T  
 C  
 C

QY 121 CGACATCAGCAGTGGAAATCGCTGGTCGTT

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; LENGTH: 925
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Proteinase Inhibitor-like promoter
US-10-039-836A-3

Query Match      6.4%; Score 59.6; DB 14; Length 925;
Best Local Similarity 59.0%; Pred. No. 4.5e-05;
Matches 138; Conservative 0; Mismatches 94; Indels 2; Gaps 2;

QY 243 AAATTATTGGCCACTTAAGGAGGTGTTTGAATGCAATAAACTAATAGTACTTGGCTAA 302
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 475 AAATCAACGCTAGACTTAATGATGCTTGAATGCAATAAACTAATAGTACTTGGCTAA 417
QY 303 AATTGTTAGTGAATATCTAGCTAACAATAGCTACCTAATTAATTAATTAATTAATTA 362
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 416 AATTAGTTGAGACATTAACACACGCTTAAATTAATTAATTAATTAATTAATTAATTA 357
QY 363 AAATAACTTATAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 422
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 356 AATTAGTTAATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAG 297
QY 423 -ACTAAGTTTATCTTTAGTGCATTAACACACGCTAATTAATTAATTAATTAATTAAT 475
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 296 AACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 243

RESULT 3
US-10-311-455-1518
; Sequence 1518, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by D
; FILE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT FILING DATE: 2002-12-16
; PRIOR FILING DATE: 2001-07-02
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1518
; LENGTH: 10328
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1518

Query Match      5.0%; Score 45.8; DB 12; Length 10328;
Best Local Similarity 46.2%; Pred. No. 0.55;
Matches 152; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

QY 192 TTCCTCTTGTGCGCAGCTGTTTCTACATTTTCAATGGCAGATATGATGAACATAATTTG 251
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2221 TTTTATTTTATATATATAAATTAACGTAAGATAAATTAAGATTTAAATTAAGA 2280
QY 252 GCCACTTAAGAGGTGTTTGAATGCAATAAACTAATAGTACTTGGCTAAATTTAG 311
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2281 TTTTAAATTAATAAATTTAGAGGAAAAAGGAAATATATTTTGGAAATATATCTTTG 2340
QY 312 TGAATTTATCTAGCTAACAATAGCTACCTAATTAATTAATTAATTAATTAATTAAT 371
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2341 GTAGAGAATTAGGATTAATTTTAAAGTAGTCTTAAAGGAAATTAATTAATTTGTAAGT 2400

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; LENGTH: 925
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Proteinase Inhibitor-like promoter
US-10-039-836A-3/C

Query Match      6.4%; Score 59.6; DB 14; Length 925;
Best Local Similarity 59.0%; Pred. No. 4.5e-05;
Matches 138; Conservative 0; Mismatches 94; Indels 2; Gaps 2;

QY 121 CGACATACGACAGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 180
QY 181 TGGCTTGAATTTCTTCTTCGACACTGTTTCTACATTTCAATGGCAGATATGATGAA 240
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 CTAATTAATTTGGCCACTTAAGGAGGTGTTTGAATGCAATAAACTAATAGTACTTGGCT 300
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 AAAATTGTTAGTGAATATCTAGCTAACAATAGCTACCTAATTAATTAATTAATTAAT 360
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 361 AAAATAACTTATAGTGAATATTAAGTGGGCTGTTTGAATGCAATAAACTAATAGTACT 420
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 361 AAAATAACTTATAGTGAATATTAAGTGGGCTGTTTGAATGCAATAAACTAATAGTACT 420
QY 421 CCACCTAACTTTATCTTTAGTGCATTAACACATGSCATAAGCTACGTTGATTTGAGAC 480
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 481 GGTAGCATCTGTCGACGAGAGATGAGCACCAGCAATCAATCTGGATAGATCGTCGCTC 540
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 541 GTGGCCGCTGTCGACGAGAGATGAGCACCAGCAATCAATCTGGATAGATCGTCGCTC 600
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 601 GTCAATCATCTGGGCTGACGGCTAATTTTCTGCACACGCACTTGAAGAGACAG 660
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 661 TCTAGGAGATGTCAAAATATATAATGCTTGGCTTCTAGCTACGTAACCTGTTGGCCT 720
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 721 GGTGTCAAGATGATCTTCAAGAAACATCTGATTTTCTCTTTCATATATTCATAT 780
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 781 TCACGCTCAGTACGCTGATGATTTGGCTTGTATTTGCTTCTTGTACAGAGATGAAC 840
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 841 GAAAGTGAAGAGCCTCCCTCGATCCCTCTCTATATATATATATATATATATATAT 900
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 901 TAGAGCCGAGGAGGAAATCTATC 925
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 901 TAGAGCCGAGGAGGAAATCTATC 925

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; Sequence 3, Application US/10039836A
; Publication No. US2003003632A1
; GENERAL INFORMATION:
; APPLICANT: Crane, Virginia
; APPLICANT: Simmons, Carl
; TITLE OF INVENTION: Maize Proteinase Inhibitor-Like
; FILE OF INVENTION: Polynucleotides and Methods of Use
; FILE REFERENCE: 35718/239836
; CURRENT APPLICATION NUMBER: US/10/039,836A
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/243,167
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3

```

Qy 372 ATAGTTAAATTAAGTTGGCTGTTGAATGCTCAACTTAATTTAGCCACTAACTTT 431  
 Db 2401 GGGCTTTAAATTAAGATTTTGTATTTGTAATAAATTAATTAAGAAAGTTAATA 2460  
 Qy 432 TATCTTTAGTCAPTCAACATGGCATAAGTCTACGTTTGTATTTGAGACGCTAGCATCGT 491  
 Db 2461 TATAATTTATGGAATGGAGGAAATATTTGTAACGATGTATTTGATAAGGTTTAATTT 2520  
 Qy 492 GCGTACGGAACAGAACCAAAAGGATTTT 520  
 Db 2521 TCGAATTTATAAGGATTTTAAATAAATGT 2549

## RESULT 4

US-10-312-841-2/c  
 ; Sequence 2, Application US/10312841  
 ; Publication No. US20030186277A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Epigenomics AG  
 ; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC  
 ; FILE REFERENCE: E01/1208/WO  
 ; CURRENT APPLICATION NUMBER: US/10/312.841  
 ; CURRENT FILING DATE: 2002-12-30  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SEQ ID NO 2  
 ; LENGTH: 3673778  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
 ; NAME/KEY: unsure  
 ; LOCATION: (379615)  
 US-10-312-841-2

Query Match 4.8%; Score 44; DB 12; Length 3673778;  
 Best Local Similarity 53.5%; Pred. No. 33;  
 Matches 92; Conservative 0; Mismatches 80; Indels 0; Gaps 0;  
 Qy 215 ACATTTCATGCGAGATATGTATGCACTAAATTAATTTGGCCACTTAAGAGGTGTTGAAT 274  
 Db 336023 ACTTTCCAAAAAATATCCAAAAATCAAAAAATCTCAAAATATAATAAAAAA 335964  
 Qy 275 GCAATAAACTAATAGTTAGTTCGCTAAATTTCTAGTGAATATCTAGCTACAAATA 334  
 Db 335963 ACATAATAATTAATAAAATTTCAAAAAATATAAAAAATTCATAATAATAAAAAA 335904  
 Qy 335 GCTACCTAACTATTAATTAATTTACCAAAAAATTAAGTTAAATTA 386  
 Db 335903 AATAAAAAACAATAACTCTATTAATAAAAAATTAATTAATAACAATAATA 335852

## RESULT 5

US-10-311-455-812  
 ; Sequence 812, Application US/10311455  
 ; Publication No. US20030143606A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: OLEK, Alexander  
 ; APPLICANT: PIEPENBROCK, Christian  
 ; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation  
 ; FILE REFERENCE: 5013.1014  
 ; CURRENT APPLICATION NUMBER: US/10/311.455  
 ; CURRENT FILING DATE: 2002-12-16  
 ; PRIOR APPLICATION NUMBER: PCT/EP01/07537  
 ; PRIOR FILING DATE: 2001-07-02  
 ; PRIOR APPLICATION NUMBER: DE 10032529.7  
 ; PRIOR FILING DATE: 2000-06-30  
 ; PRIOR APPLICATION NUMBER: DE 10043826.1  
 ; PRIOR FILING DATE: 2000-09-01  
 ; NUMBER OF SEQ ID NOS: 2424

; SEQ ID NO 812  
 ; LENGTH: 9524  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
 US-10-311-455-812

Query Match 4.7%; Score 43.6; DB 12; Length 9524;  
 Best Local Similarity 46.9%; Pred. No. 1.9;  
 Matches 136; Conservative 0; Mismatches 154; Indels 0; Gaps 0;  
 Qy 189 ATTTCTTCTTGTGCGCACCTTTCTACATTTTCATTTGGCAGATATGTATGAACATAAATA 248  
 Db 99 ATTTTCTTCTTGTGCGCACCTTTCTACATTTTCATTTGGCAGATATGTATGAACATAAATA 158  
 Qy 249 TTGGCCACTTAAGGAGGTGTTGAATGCAATAAACTAAATAGTTAGTTGGCTAAATTTGT 308  
 Db 159 TTAATTTAGTAGTGGTTATTTTAGATTTTGTAGTAAATTTAGTTTAAAGTTTATTTGGTTAA 218  
 Qy 309 TAGTGAATATCTAGTAACTAACTACCTAACTATTAACATAATTTACCAAAAAATAA 368  
 Db 219 TTGTGATTTTGTGTTAGTATAAGAGGTGAGAGTATGTGTAATAATATATGTATAGGA 278  
 Qy 369 CTTATAGTTAAATTAAGTTGGCTGTTGAATGCTCAACTAAATTTAGCCACTTAAC 428  
 Db 279 GTTATGGAAGAGGAGAAATTTAAGAAATTAATATTTATGAAAAATTTTATGATGATTTT 338  
 Qy 429 TTTTATCTTTAGTGCATTCACAACTAGCATAAGTCTACGTTTGTATTTGAG 478  
 Db 339 TTTTATCTTTAGTGCATTCACAACTAGCATAAGTCTACGTTTGTATTTGAG 388

## RESULT 6

US-10-240-485-48/c  
 ; Sequence 48, Application US/10240485  
 ; Publication No. US20030148327A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: OLEK, Alexander  
 ; APPLICANT: PIEPENBROCK, Christian  
 ; TITLE OF INVENTION: Diagnosis of Diseases Associated with Metastasis  
 ; FILE REFERENCE: 5013.1007  
 ; CURRENT APPLICATION NUMBER: US/10/240.485  
 ; CURRENT FILING DATE: 2002-10-02  
 ; PRIOR APPLICATION NUMBER: PCT/EP01/03970  
 ; PRIOR FILING DATE: 2001-04-06  
 ; PRIOR APPLICATION NUMBER: DE 10019058.8  
 ; PRIOR FILING DATE: 2000-04-06  
 ; PRIOR APPLICATION NUMBER: DE 10019173.8  
 ; PRIOR FILING DATE: 2000-04-07  
 ; PRIOR APPLICATION NUMBER: DE 10032529.7  
 ; PRIOR FILING DATE: 2000-06-30  
 ; PRIOR APPLICATION NUMBER: DE 10043826.1  
 ; PRIOR FILING DATE: 2000-09-01  
 ; NUMBER OF SEQ ID NOS: 202  
 ; SEQ ID NO 48  
 ; LENGTH: 18817  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
 US-10-240-485-48

Query Match 4.6%; Score 42.6; DB 12; Length 18817;  
 Best Local Similarity 48.2%; Pred. No. 5;  
 Matches 120; Conservative 0; Mismatches 129; Indels 0; Gaps 0;  
 Qy 218 TTTCATTTGGCAGATATGTATGAACATAATTTAGCCACTTAAGAGGTGTTGAATGCA 277  
 Db 12932 TTTCATTTCTTTATTTTCTTCAAAACTTAATAACAATAAATTTATTTAAAAA 12873

278	ATATAACTAATAGTTAGTTGGCTAAATTTGTTAGTGAATTTATCTAGCTACAAATAGCT	337
QY		
Db		
12872	AAAAAAAACACATATTTAAATAAAAAAAAATAAATACTATTCAACTCTCACCAAAA	12813
QY		
Db		
338	ACCTACTATTAACTAATTTACCAAAAATACTTATAGTTAAATTTATAGTTGGGCTGT	397
QY		
Db		
12812	ACAAACGAATCCTTTACTAAAAAAAATTTCTAATAAATTCGAAACCATATAAATCTT	12753
QY		
Db		
398	TGGAATGTCTCAACTAATTTTTAGCCACTAACTTTTATCTTTAGTGCATTCACCAATGGCA	457
QY		
Db		
12752	CAAAATTACCAAAATAAATTAAACCAATTTTCATCATTTTCCAACTATAACACAAACA	12693
QY		
Db		
458	TAAGCTCTAC	466
QY		
Db		
12692	AAAAACTAC	12684
QY		
Db		

```

RESULT 7
US-10-311-455-1048
? Sequence 1048, Application US/10311455
? Publication No. US20030143606A1
? GENERAL INFORMATION:
? APPLICANT: OLEK, Alexander
? APPLICANT: PIEPENBROCK, Christian
? APPLICANT: BERLIN, Kurt
? TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining the Methylation of Cytosine
? TITLE OF INVENTION: cytosine methylation
? FILE REFERENCE: 5013.1014
? CURRENT APPLICATION NUMBER: US/10/311,455
? CURRENT FILING DATE: 2002-12-16
? PRIOR APPLICATION NUMBER: PCT/EP01/07537
? PRIOR FILING DATE: 2001-07-02
? PRIOR APPLICATION NUMBER: DE 10032529.7
? PRIOR FILING DATE: 2000-06-30
? PRIOR APPLICATION NUMBER: DE 10043826.1
? PRIOR FILING DATE: 2000-09-01
? NUMBER OF SEQ ID NOS: 2424
? SEQ ID NO 1048
? LENGTH: 10254
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? FEATURE:
? NAME/KEY: unsure
? LOCATION: 5274, 6551, 9520
? OTHER INFORMATION: n is a or g or c or t
US-10-311-455-1048

```

Query Match.	4.6%	Score 42.2;	DB 12;	Length 10254;
Best local Similarity	48.2%;	Pred. No. 4.6;		
Matches 119;	Conservative	0;	Mismatches 128;	Indels 0; Gaps 0;
QY	229	GATATGTCGAACTAAATATATGCGCCACTTTAAGCGAGGTGTTTGAATGCAATAAAAACTAAT	288	
Db	8285	GGTATATTTGCAAGAAGATAAAAAATGTTATGTTAATGAAATGATTAAATATATATATAAAAT	8344	
QY	289	AGTTAGTTGGCTAAAATTTGTAGTGAATATATCTAGCTAACAAATAGCTACCTAACTATT	348	
Db	8345	AAAAGTAGAAAGGTTTATTTTTTGTAGTATAGAGAAAGTTAATATATTTATTAAAT	8404	
QY	349	AACTAAATTTACCAAAAATACCTTATATAGTTAAATTTATTAAGTTGGCGTGTTTGAATGCTC	408	
Db	8405	AAATTTATATATATATATATATATATGTTATTTATTTATATATATAGGTTTTTTATTAATTTTA	8464	
QY	409	AACTAAATTTAGCCACTAACTTTTATCTTTAGTGCATTCAAACATGGCATAAGCTACGT	468	
Db	8465	AAAATTTGGAAATAAATAAAATTTGATATTAATTTATTCAGATAGGTAAGAAGATGTTTGT	8524	
QY	469	TTGATTT	475	
Db	8525	TTTATTT	8531	

```

RESULT 8
US-10-240-485-152
; Sequence 152, Application US/10240485
; Publication No. US20030148327A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; TITLE OF INVENTION: Metastasis
; FILE REFERENCE: 5013.1007
; CURRENT APPLICATION NUMBER: US/10/240,485
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/03970
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 202
; SEQ ID NO 152
; LENGTH: 7676
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo s
US-10-240-485-152

```

	Query Match	4.5%	Score 41.6;	DB 12;	Length 7676;
	Best Local Similarity	53.8%;	Pred. No. 5.6;		
	Matches	Conservative	0;	Mismatches	Gaps
QY	287	ATAGTTAGTGGCTAAAATTGTTAGTCGAATAATTAATCAGCTACCAAAATAGCTACTACTA	346		
Dd	1244	AAGTAGTTTGTTTATAGTTTTAGAGATTAATGTGCAAGAATTTTTTGTGATGATTAATA	1303		
QY	347	TTAACATAATTACCAAAAATAACCTTATAGTTAAATATTAAAGTTGGCGTCTTTGAATGTC	406		
Dd	1304	TTTAAATAATTAAATCAATTAATTTGTTTGAATAGAAATATTTTGAATTGTTAAATTAT	1363		
QY	407	TCAACTAAATTTAGCCACTAACCTTTTATCTTTTAGTGCATT	446		
Dd	1364	TTTATATATTTTTTATATAAATTTTTTGTGTTTATATAAT	1403		

```

RESULT 9
US-10-311-455-1999
; Sequence 1999, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by C
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1999
; LENGTH: 17594
; TYPE: DNA

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```
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1999

Query Match      4.5%; Score 41.4; DB 12; Length 17594;
Best Local Similarity 51.5%; Pred. No. 9.8;
Matches 119; Conservative 0; Mismatches 111; Indels 1; Gaps 1;

QY 212 TCTACATTCATGCGCAGATATGTATGACATAAATTTATGGCCACCTAAGGAGGTGTTG 271
Db 845 TGTATATATAGTTTAAATATATATAATAAATTTATAAATTTGATAAATTAAGTAAGTGTGTTT 904
QY 272 AATGCAATAAACTAATAGTACTGCTGCTAAATGCTTAGTGAATTAATCTAGCTAACAA 331
Db 905 GATTTAATAAAATATAGATATTTAGTTAAATTTTAAATTTTAAATATAGTATATATTT 964
QY 332 ATAGC-TACTACTACTAATTAACCAAAATTAACCTATATAGTTAAATTTAATTAAGTT 390
Db 965 TTAGGATAAGTATGTTATAAATTTCTATGGAATATATAAATAAATTTATTTATGCTTTT 1024
QY 391 GGGCTGTTTGAATGCTCACTAAATTTTAGCCCACTAATCTTTATCTTTAGT 441
Db 1025 TTGAAATTTAAATTTAGTGTAGTATTTTGTATTTATTTGGGAAATTTAAT 1075

RESULT 10
US-10-311-455-524/c
/ Sequence 524, Application US/10311455
/ Publication No. US20030143606A1
/ GENERAL INFORMATION:
/ APPLICANT: OLEK, Alexander
/ APPLICANT: PIEPENBROCK, Christian
/ APPLICANT: BERLIN, Kurt
/ TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determination of Cytosine Methylation
/ FILE OF INVENTION: 5013.1014
/ CURRENT APPLICATION NUMBER: US/10/311,455
/ PRIOR FILING DATE: 2002-12-16
/ PRIOR APPLICATION NUMBER: PCT/EP01/07537
/ PRIOR FILING DATE: 2001-07-02
/ PRIOR APPLICATION NUMBER: DE 10032529.7
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: DE 10043826.1
/ NUMBER OF SEQ ID NOS: 2424
/ SEQ ID NO 524
/ LENGTH: 6275
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-524

Query Match      4.5%; Score 41.2; DB 12; Length 6275;
Best Local Similarity 52.3%; Pred. No. 6.4;
Matches 91; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 279 TAAACTAATAGTTAGTTGGCTAAATTTCTTAGTGAATTTATCTAGCTAACAAATAGCTA 338
Db 3387 TAAAAAATTTTAAACTTTAAATAACATTTTATTTTAAATCTCTTTTAAATAAACTATATA 3328
QY 339 CTAATACTAATTAATTAACAAATAAATATAGTAAATTTAATTTAGTTGGCTGTT 398
Db 3327 CAAAAATATTTTACATACATAAATAATATACCTCTCTTTTAACTCACTACITTTCTTA 3268
QY 399 TGAATGCTCACTAATTTTAGCCCACTAATTTTATCTTTTAGTGCATTCACACA 452
Db 3267 TTTATATCAAAACATTTTAAACAAACAAACTATCCCTAAATCATATAACA 3214

RESULT 11
US-10-311-455-1429
```

```
/ Sequence 1429, Application US/10311455
/ Publication No. US20030143606A1
/ GENERAL INFORMATION:
/ APPLICANT: OLEK, Alexander
/ APPLICANT: PIEPENBROCK, Christian
/ APPLICANT: BERLIN, Kurt
/ TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determination of Cytosine Methylation
/ FILE OF INVENTION: 5013.1014
/ CURRENT APPLICATION NUMBER: US/10/311,455
/ PRIOR FILING DATE: 2002-12-16
/ PRIOR APPLICATION NUMBER: PCT/EP01/07537
/ PRIOR FILING DATE: 2001-07-02
/ PRIOR APPLICATION NUMBER: DE 10032529.7
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: DE 10043826.1
/ NUMBER OF SEQ ID NOS: 2424
/ SEQ ID NO 1429
/ LENGTH: 5488
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1429

Query Match      4.4%; Score 41; DB 12; Length 5488;
Best Local Similarity 55.2%; Pred. No. 6.8;
Matches 80; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 302 AAATGTTAGTGAATTAATCTAGCTAACAAATAGCTAGCTAATTAATTAATTAATTAAT 361
Db 1615 AAATGATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1674
QY 362 AAATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 421
Db 1675 AATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1734
QY 422 CACTAATCTTTATCTTAGTGCAAT 446
Db 1735 ATTTATTTATATTTGTAGTGT 1759

RESULT 12
US-10-311-455-1368/c
/ Sequence 1368, Application US/10311455
/ Publication No. US20030143606A1
/ GENERAL INFORMATION:
/ APPLICANT: OLEK, Alexander
/ APPLICANT: PIEPENBROCK, Christian
/ APPLICANT: BERLIN, Kurt
/ TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determination of Cytosine Methylation
/ FILE OF INVENTION: 5013.1014
/ CURRENT APPLICATION NUMBER: US/10/311,455
/ PRIOR FILING DATE: 2002-12-16
/ PRIOR APPLICATION NUMBER: PCT/EP01/07537
/ PRIOR FILING DATE: 2001-07-02
/ PRIOR APPLICATION NUMBER: DE 10032529.7
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: DE 10043826.1
/ NUMBER OF SEQ ID NOS: 2424
/ SEQ ID NO 1368
/ LENGTH: 5930
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1368

Query Match      4.4%; Score 41; DB 12; Length 5930;
Best Local Similarity 49.8%; Pred. No. 7;
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	Matches	104;	Conservative	0;	Mismatches	105;	Indels	0;	Gaps	0;
Qy	230	ATATGTATGAAC	TAAATATTTTGGCCACTTAAGGAGGTGTTTGAATGCAATAAACAACTAATA	289						
Db	5093	AAATTTAAAAAC	TAAATTCCTAAAAATCTAAATATATTAACATATATAAATPAAAAATAAAAA	5034						
Qy	290	GTTAGTTGGCTA	AAAAATTTGTGTAGTGAATATCTAGCTAACAAATAGCTAAGCTAATCTAATTA	349						
Db	5033	AATAAAAAAAC	TTTCATTTTACTTTATTTCTATACTTTAAAAAATACTTAAAAACGTATA	4974						
Qy	350	ACTAATTTTACCA	AAAAAATACTTATAGTATAATATTAAAGTTGGCGCTGTTTGAATGTCCTCA	409						
Db	4973	TTATTTTATAATA	ATAATACATTTAATACAAAATTTCAATATTAATTTTCTCAAAAAATTT	4914						
Qy	410	ACTAATTTTAGCC	AACTATTTTATCTTT	438						
Db	4913	ACAAATTTAAAA	CTTTAAAAATTTTATTT	4885						

RESULT 13  
 US-10-270-839-108/c  
 ; Sequence 108, Application US/10270839  
 ; Publication No. US20030143586A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chao, Qimin  
 ; APPLICANT: Grasso, Luigi  
 ; APPLICANT: Sass, Philip M.  
 ; APPLICANT: Nicolaïdes, Nicholas C.  
 ; TITLE OF INVENTION: Genetic Hypermethylability of Plants for Gene Discovery and Diagnosis  
 ; FILE REFERENCE: AG000205 (WOR-0133)  
 ; CURRENT APPLICATION NUMBER: US/10/270, 839  
 ; CURRENT FILING DATE: 2002-10-11  
 ; PRIOR APPLICATION NUMBER: 60/328,750  
 ; PRIOR FILING DATE: 2001-10-12  
 ; NUMBER OF SEQ ID NOS: 129  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 108  
 ; LENGTH: 88  
 ; TYPE: DNA  
 ; ORGANISM: *Conyza sp.*  
 US-10-270-839-108

	Query Match	4.4%	Score 40.8	DB 12	Length 88
	Best Local Similarity	75.0%	Pred. No. 0.88		
	Matches 51	Conservative 0	Mismatches 17	Indels 0	Gaps 0
QY	1	ACTATAGGCACCGCTGGTGCAGCGCCGGCTGGTGTATTGTGTCCAAACATTTTGA	60		
Db	88	ACTTAAGGCGACCGCTGGTGCAGCGCCGGCTGGTGTATTTTACATACAACCTAT	29		
QY	61	TGTGTATGG	68		
Db	28	TCAGATCG	21		

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RESULT 14
US-09-938-842A-5309/c
; Sequence 5309, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16

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; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 5309
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-338-842A-5309

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Query Match.	4.4%;	Score 40.6;	DB 10;	Length 2000;
Best Local Similarity	50.8%;	Pred. No. 5.1;		
Matches 97;	Conservative 0;	Mismatches 94;	Indels 0;	Gaps 0;
QY	215	ACATTTTCATTGGCAGATATGATGCACTCAATATATTGGCCACITAAAGGAGGTGTTCGAAT	274	
Db	1728	ATATATATGGATAATGCAAGCTGACTTATATATAGATCAATTAAAGCTTTATTATTGAAT	1669	
QY	275	GCAATAAACCTAATAGTTAGTTGGCTGAAAATGTTAGTGAATATATCTAGCTAACCAATA	334	
Db	1668	TCAATCAAAATTATAATATATACTAAATATATAAACTTTTAATTATCTATATAATTAAAA	1609	
QY	335	GCTACCTTAACCTAATTAACTAATTTACCAAAAATAACTTTATAGTTAAATTTATAGTTGGGC	394	
Db	1608	TTTTGCAATGAATTAATTAATTCATCTATATACTTATATATATATATACACTTATATA	1549	
QY	395	TGTTTGAATGT	405	
Db	1548	TATTTGATTC	1538	

## RESULT 15

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US-10-311-455-1571
; Sequence 1571, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by D
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1571
; LENGTH: 5487
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1571

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	Query Match	4.4%	Score 40.6;	DB 12;	Length 5487;		
	Best local similarity	56.3%;	Pred. No. 8.6;				
	Matches	76;	Conservative	0;	Mismatches		
				59;	Indels		
				0;	Gaps		
QY	273	ATCCCAATAA	AACTAAATAGT	TAGTGGCT	AAAAATGTTAGTGA	AAATATCTAGCTACAAA	332
Db	495	ATTTAATTTAA	ATAAATAATAT	ATTTAAATTA	ATTAATTTAA	ATAATATTTAAAGATAAATAA	554
QY	333	TAGCTACCTA	AACTATTAACT	ATTTCCAAAA	TAACTATATCT	TATTAATTTATTAAGTTGG	392
Db	555	TATATAATTA	TATATAATAA	ATTTATATAA	TATATAATTA	TAAATTAATTAATTTATAAATAATA	614
QY	393	GCTGTTTGA	ATGTC	407			
Db	615	GATTTATAA	ATTTT	629			

Fri Oct 17 11:56:06 2003

us-10-039-836a-3.rnpb

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Search completed: October 17, 2003, 11:44:17  
Job time : 248 secs

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## RESULT 4



; TITLE OF INVENTION: A No. 6171857el Leucine zipper, KARP-1 and  
; TITLE OF INVENTION: Methods of Regulating DNA Dependent Protein Kinase Activity  
; FILE REFERENCE: B0877/7017/HK

; CURRENT APPLICATION NUMBER: US/09/173,914

; CURRENT FILING DATE: 1998-10-16

; EARLIER FILING DATE: 1997-10-17

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 6078

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (178)...(178)

; NAME/KEY: unsure

; LOCATION: (230)...(230)

; NAME/KEY: unsure

; LOCATION: (232)...(232)

; NAME/KEY: unsure

; LOCATION: (234)...(234)

; NAME/KEY: unsure

; LOCATION: (453)...(453)

; NAME/KEY: unsure

; LOCATION: (473)...(473)

; NAME/KEY: unsure

; LOCATION: (610)...(610)

; NAME/KEY: unsure

; LOCATION: (612)...(612)

; NAME/KEY: unsure

; LOCATION: (2175)...(2175)

; NAME/KEY: unsure

; LOCATION: (1014)...(1014)

US-09-173-914-1

US-09-173-914-1

US-09-173-914-1

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US-09-173-914-1





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;
; OTHER INFORMATION: score 1.000
; OTHER INFORMATION: sequence TGTGTCGTC
US-08-905-223-37

Query Match
Best Local Similarity 4.1%; Score 37.8; DB 3; Length 555;
Matches 39; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 CTTAGGGCACGGTGGTGCACGGCCGGCGTGGTGTATTGTG 46
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 CTTAGGGCACGGKTTGGTGCACGGCCGGCGTGGTGTCTGTG 45

RESULT 15
US-09-247-155-37
; Sequence 37, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET 021A
; CURRENT APPLICATION NUMBER: US/09/247,155A
; CURRENT FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/074,121
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/081,563
; EARLIER FILING DATE: 1998-04-13
; EARLIER APPLICATION NUMBER: 60/096,116
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/099,273
; EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm
; SEQ ID NO 37
; LENGTH: 555
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: promoter
; LOCATION: 1..500
; FEATURE:
; OTHER INFORMATION: codon_start="501"
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: 191..206
; OTHER INFORMATION: matinspector prediction
; OTHER INFORMATION: name ARN1_01
; OTHER INFORMATION: score 0.964
; OTHER INFORMATION: sequence ggactcacgtgtgtgct
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: 193..204
; OTHER INFORMATION: matinspector prediction
; OTHER INFORMATION: name NM1C_01
; OTHER INFORMATION: score 0.965
; OTHER INFORMATION: sequence actcaactgtgtg
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: 193..204
; OTHER INFORMATION: matinspector prediction
; OTHER INFORMATION: name USF_01
; OTHER INFORMATION: score 0.985
; OTHER INFORMATION: sequence actcacgtgtgctg
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: complement(193..204)
; OTHER INFORMATION: matinspector prediction
; OTHER INFORMATION: name USF_01
; OTHER INFORMATION: score 0.985
; OTHER INFORMATION: sequence cagcacgtgagtg
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: complement(193..204)
; OTHER INFORMATION: matinspector prediction
; OTHER INFORMATION: name NM1C_01
; OTHER INFORMATION: score 0.956
; OTHER INFORMATION: sequence cagcacgtgagtg
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: complement(193..204)
; OTHER INFORMATION: matinspector prediction
; OTHER INFORMATION: name MYCMA_02
; OTHER INFORMATION: score 0.972
; OTHER INFORMATION: sequence cagcacgtgagtg
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: 195..202
; OTHER INFORMATION: matinspector prediction
; OTHER INFORMATION: name USF_C
; OTHER INFORMATION: score 0.997
; OTHER INFORMATION: sequence tcaactgtgc
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: complement(195..202)
; OTHER INFORMATION: matinspector prediction
; OTHER INFORMATION: name USF_C
; OTHER INFORMATION: score 0.991
; OTHER INFORMATION: sequence gcaactgtga
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: complement(210..217)
; OTHER INFORMATION: matinspector prediction
; OTHER INFORMATION: name M2F1_01
; OTHER INFORMATION: score 0.968
; OTHER INFORMATION: sequence catgggga
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: 397..410
; OTHER INFORMATION: matinspector prediction
; OTHER INFORMATION: name ELK1_02
; OTHER INFORMATION: score 0.963
; OTHER INFORMATION: sequence ctctccggaagcct
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: 400..409
; OTHER INFORMATION: matinspector prediction
; OTHER INFORMATION: name CETSIP54_01
; OTHER INFORMATION: score 0.974
; OTHER INFORMATION: sequence tccggaagcc
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: complement(460..470)
; OTHER INFORMATION: matinspector prediction
; OTHER INFORMATION: name API_04
; OTHER INFORMATION: score 0.963
; OTHER INFORMATION: sequence agtgactgaac
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: complement(460..470)
; OTHER INFORMATION: matinspector prediction
; OTHER INFORMATION: name APIFJ_02
; OTHER INFORMATION: score 0.961
; OTHER INFORMATION: sequence agtgactgaac
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: 547..555
; OTHER INFORMATION: matinspector prediction
; OTHER INFORMATION: name PADS_C
; OTHER INFORMATION: score 1.000
; OTHER INFORMATION: sequence tgtgtgtctc
; US-09-247-155-37

Query Match 4.1%; Score 37.8; DB 4; Length 555;
Best Local Similarity 86.7%; Pred. No. 0.26;
US-09-247-155-37
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Matches	39;	Conservative	2;	Mismatches	4;	Indels	0;	Gaps	0;
Qy	2	CTATAGGGCACGCGTGGTCGACGCGCCCGGCTGGTCGTATTGTG	46						
Db	1	CTATAGGGCACGCKTGGTCGACGCGCCCGGCTGGTCGTGTK	45						

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 Job time : 67 secs